RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/031,331C_

Source: _1FW16_

Date Processed by STIC: _12/21/04_

ENTERED

RAW SEQUENCE LISTING   DATE: 12/21/2004
PATENT APPLICATION: US/10/031,331C   TIME: 14:42:39

Input Set : **A:\yamada sequence listing.txt**
Output Set: **N:\CRF4\12212004\J031331C.raw**

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 3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY CORPORATION
 5 <120> TITLE OF INVENTION: Screening of genes to give tolerance against
 6       environmental stress and the apprications
 8 <130> FILE REFERENCE: YG12-12PCT
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C--> 10 **<140> CURRENT APPLICATION NUMBER: US/10/031,331C**
C--> 11 **<141> CURRENT FILING DATE: 2002-01-18**
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13 <150> PRIOR APPLICATION NUMBER: JP P1999-235910
14 <151> PRIOR FILING DATE: 1999-07-19
16 <150> PRIOR APPLICATION NUMBER: JP P2000-85377
17 <151> PRIOR FILING DATE: 2000-03-24
19 <160> NUMBER OF SEQ ID NOS: 72
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1018
25 <212> TYPE: DNA
26 <213> ORGANISM: Bruguiera sexangula
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (42)..(464)
32 <400> SEQUENCE: 1
33 gtccaaacag ccagagagaa acgacaacat cgaccaagaa a atg gct ctt tca agc 56
34                                                Met Ala Leu Ser Ser
35                                                 1               5
37 tct gct ctg aga acc gtc tct tct tct gtg aag gtg gtc ggc cct gca   104
38 Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys Val Val Gly Pro Ala
39                  10              15                  20
41 aga tca aag agt gct act gta ccc acc caa aca gta ttg cct ttc aag   152
42 Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys
43              25              30              35
45 ttc aca aac ccg tcg tta ctc act cga tcg cta agc ttt tca tca aaa   200
46 Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu Ser Phe Ser Ser Lys
47          40              45              50
49 ggt tca agc ttt gac agc ttc tct gta ccc aaa aga tct ttt tct tgc   248
50 Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys Arg Ser Phe Ser Cys
51      55              60              65
53 aga agc caa gcc act cca tct gat gat gcc tca aga ccc acc aaa gtt   296
54 Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val
55   70              75              80                  85
57 caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct   344
58 Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro
59              90              95                  100
61 gct gtt ctc cgg ttg agc cag aaa cct gtt aat tct ctc ggc gat ctc   392
62 Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu
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63                105              110              115
65 gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att   440
66 Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile
67            120              125              130
69 gga gta acc gca gaa tat gca tcc tgatccaaaa caagccagaa aaaaagggtg   494
70 Gly Val Thr Ala Glu Tyr Ala Ser
71      135                140
73 atcgctttga agcgatatat agcttttatt tcggtggcta tggtcacatt gctgtgcaag 554
75 gcgcatactt gacctacgag gacacgcacc ttgctgtgac gggcgggtcg ggcatatttg 614
77 aaggagtgtc tggtcaggtt aagctgcagc aactcgtgta ccctttcaag ctcttctaca 674
79 ctttctactt gcgaggcatc aaggacttgc cggaggagct tacgaagaag ccggttgagc 734
81 cccacccttc tgttgagccg atgccggcgg ccaaggcttg cgagccacat gccgttgttg 794
83 ctaatttcac cgattagtga ttaattgtcc tttttggggtt cggatgaact tgagttagct 854
85 tacagttgca caacgttatg gcgcgagaca cgagagggaa ccttagccat aagaaaatta 914
87 ataatctcac ggtgctttta ttttgattct tctattagtt gaatcgttaa tgaaagtgga 974
89 ccaaattggc tgttttacgt tttaaaaaaa aaaaaaaaaa aaaa              1018
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 141
94 <212> TYPE: PRT
95 <213> ORGANISM: Bruguiera sexangula
97 <400> SEQUENCE: 2
98 Met Ala Leu Ser Ser Ser Ala Leu Arg Thr Val Ser Ser Ser Val Lys
99   1               5                  10                  15
101 Val Val Gly Pro Ala Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr
102            20                  25                  30
104 Val Leu Pro Phe Lys Phe Thr Asn Pro Ser Leu Leu Thr Arg Ser Leu
105            35                  40                  45
107 Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys
108        50                  55                  60
110 Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser
111   65                  70                  75                  80
113 Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
114                85                  90                  95
116 Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn
117            100                 105                 110
119 Ser Leu Gly Asp Leu Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp
120            115                 120                 125
122 Leu Gln Lys Arg Ile Gly Val Thr Ala Glu Tyr Ala Ser
123        130                 135                 140
127 <210> SEQ ID NO: 3
128 <211> LENGTH: 2060
129 <212> TYPE: DNA
130 <213> ORGANISM: Bruguiera sexangula
132 <220> FEATURE:
133 <221> NAME/KEY: CDS
134 <222> LOCATION: (81)..(1718)
136 <400> SEQUENCE: 3
137 cgaaattcct ctactaacaa taccagatcc agtctagcgt ttcgattttc tgcttcacat 60
139 ttctgtttct ttgaccagaa atg gca atc gcg gct caa act ccg gac att ctc 113
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140                         Met Ala Ile Ala Ala Gln Thr Pro Asp Ile Leu
141                         1 \               5                    10
143 ggc gaa cgt cag tcc ggc cag gac gtc cgc act caa aat gtg gtg gca    161
144 Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala
145           15                  20                  25
147 tgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga    209
148 Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly
149           30                  35                  40
151 ctc gac aag atg cta gtg gat gat att ggt gat gta aca att aca aat    257
152 Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn
153       45                  50                  55
155 gat ggt gct acg att ctt aag atg tta gaa gta gag cat cct gca gca    305
156 Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala
157 60                  65                  70                  75
159 aag gtg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat    353
160 Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp
161                 80                  85                  90
163 gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca    401
164 Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala
165                 95                  100                 105
167 aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga    449
168 Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly
169           110                 115                 120
171 tac agg ctt gct atg agg gaa gca tgc aag tat gtt gaa gag aaa ttg    497
172 Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu
173       125                 130                 135
175 tca atg aag gtt gaa aag ctt gga aaa gat tct cta gta aac tgt gca    545
176 Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala
177 140                 145                 150                 155
179 aag aca agc atg tcc tca aag ttg ata gct ggt gac agc gac ttc ttt    593
180 Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe
181                 160                 165                 170
183 gca aat ttg gtt gta gat gct gta caa gca gta aag atg acc aat gca    641
184 Ala Asn Leu Val Val Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala
185                 175                 180                 185
187 cgg ggg gaa atc aaa tat cct atc aag agt ata aat att ttg aaa gct    689
188 Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala
189           190                 195           .     200
191 cat gga aaa agt gca aga gat agc tgc ctt ttg aat ggc tat gct ctc    737
192 His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu
193       205                 210                 215
195 aat act ggt cgt gct gct caa ggg atg cct atg aga gtt gca cct gca    785
196 Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala
197 220                 225                 230                 235
199 agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg    833
200 Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu
201                 240                 245                 250
203 ggt gta caa gtc tta gtc act gat ccc agg gag ctt gaa aga att cgt    881
204 Gly Val Gln Val Leu Val Thr Asp Pro Arg Glu Leu Glu Arg Ile Arg
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205                 255                 260                 265
207 caa aga gaa gct gat atg aca aag gaa cgg att gag aaa ctc ctg aaa     929
208 Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys
209           270                 275                 280
211 gct gga gca aat gtt gtt cta acc aca aag gga att gat gac atg gca     977
212 Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala
213     285                 290                 295
215 ctt aaa tat ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg     1025
216 Leu Lys Tyr Phe Val Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg
217 300                 305                 310                 315
219 aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt     1073
220 Lys Glu Asp Met Arg His Val Ala Lys Ala Thr Gly Ala Thr Leu Val
221           320                 325                 330
223 tca aca ttt gct gac atg gaa gga gag gaa aca ttt gat tca tca ctg     1121
224 Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu
225     335                 340                 345
227 ctt gga caa gct gaa gaa gtt gtg gag gag cgc att gct gat gac gat     1169
228 Leu Gly Gln Ala Glu Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp
229           350                 355                 360
231 gtg att atg ata aaa ggg aca aag act aca agt gcg gtt tcc ttg att     1217
232 Val Ile Met Ile Lys Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile
233     365                 370                 375
235 ctt cgt ggt gca aat gac tat atg ctc gat gag atg gag cga gcc ctg     1265
236 Leu Arg Gly Ala Asn Asp Tyr Met Leu Asp Glu Met Glu Arg Ala Leu
237 380                 385                 390                 395
239 cat gat gct tta tgt att gtc aag aga acc ctt gaa tct aat aca gta     1313
240 His Asp Ala Leu Cys Ile Val Lys Arg Thr Leu Glu Ser Asn Thr Val
241           400                 405                 410
243 gtt gca ggt gga ggt gct gtt gag gct gcc ttg tct gtg cac ttg gag     1361
244 Val Ala Gly Gly Gly Ala Val Glu Ala Ala Leu Ser Val His Leu Glu
245           415                 420                 425
247 tac ctc gct aca act ctt ggg tca cga gag cag tta gca ata gca gag     1409
248 Tyr Leu Ala Thr Thr Leu Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu
249           430                 435                 440
251 ttt gca gaa tcc ttg ttg att ata cca aag gtt ctt gct gtc aat gct     1457
252 Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala
253     445                 450                 455
255 gcc aaa gat gcc act gaa tta gct gca aaa ctc cgg gct tac cac cat     1505
256 Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His
257 460                 465                 470                 475
259 aca gca caa aca aag gct gat aag aaa cat tta tca agc atg gga cta     1553
260 Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu
261           480                 485                 490
263 gac ctt tca aag ggg acc atc cga aac aac tta gaa gct gga gtc att     1601
264 Asp Leu Ser Lys Gly Thr Ile Arg Asn Asn Leu Glu Ala Gly Val Ile
265           495                 500                 505
267 gaa cct gca atg agc aaa ata aag ata att cag ttt gct act gaa gca     1649
268 Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala
269     510                 515                 520
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271 gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat    1697
272 Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp
273     525               530           535
275 gag act cag aat gaa gag gaa tagatgcaga ctcttgtaag ctgcctccct        1748
276 Glu Thr Gln Asn Glu Glu Glu
277 540               545
279 tttgttttca aatttgtgtc ccttgcgagc tggaggaaag ggggggtgtt tatgtggtgt 1808
281 tttcagtggt tttaattttt caaggagctc gcggcctgtg tactttaggt tagagtccat 1868
283 ccaaggggtg tttattggat aatgcctaag ctgtttctcg tctattagta ggctggtagt 1928
285 tccactgagt tctcatccca attaaaagaa tgagatcaaa gggtcctaaa ttcgtactca 1988
287 ttggtgcacg atttgtttct gacaagcata agacttgacc ctctctatca caataaaaaa 2048
289 aaaaaaaaaa aa                                                       2060
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 546
294 <212> TYPE: PRT
295 <213> ORGANISM: Bruguiera sexangula
297 <400> SEQUENCE: 4
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299   1                 5                   10                  15
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302             20                  25                  30
304 Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly Leu Asp Lys Met Leu
305             35                  40                  45
307 Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn Asp Gly Ala Thr Ile
308         50                  55                  60
310 Leu Lys Met Leu Glu Val Glu His Pro Ala Ala Lys Val Leu Val Glu
311 65                  70                  75                  80
313 Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp Gly Thr Thr Ser Val
314                 85                  90                  95
316 Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala Asn Asp Leu Val Arg
317             100                 105                 110
319 Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly Tyr Arg Leu Ala Met
320         115                 120                 125
322 Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu Ser Met Lys Val Glu
323     130                 135                 140
325 Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala Lys Thr Ser Met Ser
326 145                 150                 155                 160
328 Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe Ala Asn Leu Val Val
329                 165                 170                 175
331 Asp Ala Val Gln Ala Val Lys Met Thr Asn Ala Arg Gly Glu Ile Lys
332             180                 185                 190
334 Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala His Gly Lys Ser Ala
335         195                 200                 205
337 Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala
338     210                 215                 220
340 Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala Arg Ile Ala Cys Leu
341 225                 230                 235                 240
343 Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu Gly Val Gln Val Leu
344                 245                 250                 255
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VERIFICATION SUMMARY   DATE: 12/21/2004
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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date